

10/501,566

Sequence Alignments

RESULT 1

US-08-176-126B-2

; Sequence 2, Application US/08176126B

; Patent No. 5589358

; GENERAL INFORMATION:

; APPLICANT: Dawson, Paul A.

; TITLE OF INVENTION: ILEAL BILE ACID TRANSPORTER COMPOSITIONS AND

; TITLE OF INVENTION: METHODS

; NUMBER OF SEQUENCES: 5

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Arnold, White & Durkee

; STREET: P.O. Box 4433

; CITY: Houston

; STATE: Texas

; COUNTRY: US

; ZIP: 77210

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/176,126B

; FILING DATE: 29-DEC-1993

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Parker, David L.

; REGISTRATION NUMBER: 32,165

; REFERENCE/DOCKET NUMBER: WAKE:002/PAR

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (512) 418-3000

; TELEFAX: (512) 474-7577

; TELEX: na

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 348 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-176-126B-2

Query Match 44.7%; Score 884; DB 1; Length 348;

Best Local Similarity 46.9%; Pred. No. 8.9e-82;

Matches 164; Conservative 74; Mismatches 102; Indels 10; Gaps 4;

Qy 7 SSSACPANSS--EEELPVGLEVHGN--LELVFTTVVSTVMMGLLMFSLGCSVEIRKLWSHI 62
:| | | |:: | : : | : | | : | |::: |::|::|::|: | |:

Db 3 NSSICNPNATICEGDSIAPE SNFNAILSVVMSTVLTILLALVMFSGMGCNVELHKFLGHL 62

Qy 63 RRPWGIAVGLLCQFGLMPFTAYLLAISFSLKPVQAI AVLIMGCCPGGTISNIFTFWVDGD 122
| | | | | | | | | | | | | | | : | : | : | : | : | : | | | | | | | | | | | | | |

Db 63 RRPWGIVVGFLCQFGIMPLTGFVLSVAFGILPVQAVVLIQGCCPGGTASNILAYWVDGD 122

Qy	123	MDLSISMTTCSTVAALGMMPLCIYLYTWSWSLQQNLTIPIYQNIGITLVCLTIPVAFGVYV	182
		: : ::: : : : : :	
Db	123	MDLSVSMTTCSTLLALGMMPLCLFIYTKMWVDSGTIVIPYDSIGTSLVALVIPVSIGMYV	182
Qy	183	NYRWPKQSKIILKIGAVVGGVLLLVAVAGVVLAKGSWNSDITLLTISFIFPLIGHVTGF	242
		:: ::: :: : ::: : : : : : : :	
Db	183	NHKWPQKAKIILKIGSIAGAILIVLIAVVGILYQSAWTIEPKLWIIGTIYPIAGYGLGF	242
Qy	243	LLALFTHQSWQRCRTISLETGAQNIQMCITMLQLSFTAHLVQMLSFPLAYGLFQLIDGF	302
		: : : : : : : :	
Db	243	FLARIAGQPWYRCRTVALETGLQNTQLCSTIVQLSFSPEDLNLVFTFPLIYSIFQIAFAA	302
Qy	303	LIVAAYQTYKRRLKNKHGKKNSGCTEVCHTRKS--TSSRETNAFLEVNEE	350
		::: : : : : : : :	
Db	303	ILLGAYVAYKK----CHGKNNTLQEKTDNEMEPRSSFQETNKGFPDEK	348

RESULT 1
 US-10-091-628-2
 ; Sequence 2, Application US/10091628
 ; Publication No. US20020164627A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wilganowski, Nathaniel L.
 ; APPLICANT: Nepomnichy, Boris
 ; APPLICANT: Burnett, Michael B.
 ; APPLICANT: Hu, Yi
 ; TITLE OF INVENTION: No. US20020164627A1el Human Transporter Proteins and
 Polynucleotides Encoding the
 ; TITLE OF INVENTION: Same
 ; FILE REFERENCE: LEX-0314-USA
 ; CURRENT APPLICATION NUMBER: US/10/091,628
 ; CURRENT FILING DATE: 2002-03-06
 ; PRIOR APPLICATION NUMBER: US 60/275,009
 ; PRIOR FILING DATE: 2001-03-12
 ; PRIOR APPLICATION NUMBER: US 60/284,152
 ; PRIOR FILING DATE: 2001-04-17
 ; NUMBER OF SEQ ID NOS: 6
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 2
 ; LENGTH: 377
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-091-628-2

Query Match 100.0%; Score 1979; DB 4; Length 377;
 Best Local Similarity 100.0%; Pred. No. 8.1e-178;
 Matches 377; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MRANCSSSSACPANSSEEELPVGLEVHGNLELVFTVVSTVMMGLLMFSLGCSVEIRKLWS	60
Db	1	MRANCSSSSACPANSSEEELPVGLEVHGNLELVFTVVSTVMMGLLMFSLGCSVEIRKLWS	60
Qy	61	HIRRPWGIAVGLLCQFGLMPFTAYLLAISFSLKPVQAI AVLIMGCCPGGTISNIFTFWVD	120
Db	61	HIRRPWGIAVGLLCQFGLMPFTAYLLAISFSLKPVQAI AVLIMGCCPGGTISNIFTFWVD	120
Qy	121	GDMDLSISMTTCSTVAALGMMPLCIYLYTWSWSLQQNL TIPYQNIGITLVCLTIPVAFGV	180
Db	121	GDMDLSISMTTCSTVAALGMMPLCIYLYTWSWSLQQNL TIPYQNIGITLVCLTIPVAFGV	180
Qy	181	YVNYRWPKQSKIILKIGAVVGGVLLLVAVAGVVLAKGSWNSDITLLTISFIFPLIGHVT	240
Db	181	YVNYRWPKQSKIILKIGAVVGGVLLLVAVAGVVLAKGSWNSDITLLTISFIFPLIGHVT	240
Qy	241	GFLALFTHQSWQRCRTISLETGAQNIQMCITMLQLSFTAHLVQMLSFPPLAYGLFQLID	300
Db	241	GFLALFTHQSWQRCRTISLETGAQNIQMCITMLQLSFTAHLVQMLSFPPLAYGLFQLID	300
Qy	301	GFLIVAAYQTYKRRLKNKHGKKN SGCTEVCHTRKSTSSRETNAFLEVNEEGAITPGPPGP	360
Db	301	GFLIVAAYQTYKRRLKNKHGKKN SGCTEVCHTRKSTSSRETNAFLEVNEEGAITPGPPGP	360
Qy	361	MDCHRALEPVGHITSCE	377

Db

361 MDCHRALEPVGHITSCE 377